RESULT 1
AAY06483
ID AAY06483 standard; Protein; 455 AA.
XX
AC AAY06483;
XX
DT 27-SEP-1999 (first entry)
XX
DE Human tumour-associated protein PRO347.
XX
KW PRO347; UNQ306; cancer; tumour; diagnosis; therapy; human.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Peptide   1..26
FT   /note= "signal peptide"
FT Protein   27..455
FT   /note= "mature protein"
FT Modified-site   144
FT   /note= "N-glycosylated"
FT Domain   247..279
FT   /note= "EGF-like domain cysteine pattern signature"
FT Domain   280..416
FT   /note= "EGF-like domain cysteine pattern signature"
FT Domain   416..455
FT   /note= "C-type lectin domain signature"
XX
PN WO9935170-A2.
XX
PD 15-JUL-1999.
XX
PF 05-JAN-1999; 99WO-US00106.
XX
PR 20-NOV-1998; 98US-0109304.
PR 05-JAN-1998; 98US-0070440.
PR 29-APR-1998; 98US-0083500.
PR 22-MAY-1998; 98US-0086414.
PR 10-JUN-1998; 98US-0088742.
PR 10-NOV-1998; 98US-0107783.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
PI Roy MA, Wood WI;
XX
DR WPI; 1999-430385/36.
DR N-PSDB; AAX87260.
XX
PT Antibody against proteins expressed in neoplastic cells, useful for
PT tumor diagnosis and treatment
XX
PS Example 1; Fig 14; 162pp; English.
XX
CC This sequence represents human PRO347 (UNQ306), a 50.5 5 kDa protein
CC (pI 8.44) encoded by the novel cDNA clone DNA44176 (see AAX87260).
CC Amplification of DNA44176 was observed in various tumour lines,
CC suggesting a role in tumour formation and growth. Antagonists
CC (e.g. antibodies) directed to PRO347 may have use in cancer therapy.
CC The invention identifies 14 genes (see AAX87254-67) that are amplified
CC in the genome of tumour cells. Such amplification is expected to be
CC associated with overexpression of the gene product and to contribute
CC to tumorigenesis. The encoded proteins (see AAY06477-90) may be
CC useful targets for the diagnosis and/or treatment (including
CC prevention) of certain cancers, and may act as predictors of the
CC prognosis of tumour treatment. Antibodies that bind the proteins
CC are claimed and used in claimed cancer diagnostic kits.
XX
SQ Sequence 455 AA;

Query Match 100.0%; Score 2529; DB 20; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.7e-183;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60

Qy     61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120

Qy    121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180

Qy    181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240

Qy    241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300

Qy    301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360

Qy    361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420

Qy    421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
          |||||||||||||||||||||||||||||||||||
Db    421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
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Sequence Alignments

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RESULT 4
AAY41266
ID   AAY41266 standard; Protein; 446 AA.
XX
AC   AAY41266;
XX
DT   31-JAN-2000  (first entry)
XX
DE   Human T139 protein.
XX
KW   Human; T139 polypeptide; immune system disorder; spermatogenesis;
KW   sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
XX
OS   Homo sapiens.
XX
PN   WO9954343-A2.
XX
PD   28-OCT-1999.
XX
PF   23-APR-1999;   99WO-US08896.
XX
PR   23-APR-1998;   98US-0065661.
XX
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI   Holtzman D;
XX
DR   WPI; 1999-633969/54.
DR   N-PSDB; AAZ23299, AAZ23300.
XX
PT   Human T139 nucleic acids and polypeptides, useful for treating
PT   proliferative disorders associated with aberrant T139 expression or
PT   activity -
XX
PS   Claim 9; Fig 1; 115pp; English.
XX
CC   This represents a human T139 polypeptide. The T139 polypeptide can be
CC   expressed by standard recombinant methodology. The T139 cDNA insert is
CC   deposited with ATCC under accession number 98694. The T139 polypeptides
CC   and polynucleotides can be administered therapeutically or
CC   prophylactically to treat/prevent disorders associated with aberrant T139
CC   expression or activity, especially proliferative or differentiative
CC   disorders, e.g. of the immune system. They can be used to modulate
CC   spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or
CC   to treat disorders related to defects in sperm-egg fusion. They may also
CC   be useful to treat testicular disorders e.g. testicular cancer. The
CC   polypeptides may be used to identify selectively binding compounds which
CC   may be useful for detecting the polypeptides in samples; and identifying
CC   compounds modulating polypeptide activity. The polynucleotides are useful
CC   for producing probes or primers that selectively hybridize to the
CC   polynucleotides which may be useful for detecting the polynucleotides in
CC   a sample, gene mapping; identifying cells or tissues expressing aberrant
CC   T139 levels; determining if a gene has been mutated or deleted to
CC   identify subjects at risk for or having a disorder associated with T139
CC   expression or activity and to monitor therapeutic interventions; and for
CC   producing antisense sequences for therapeutic administration to modulate
CC   /prevent T139 expression.
XX
SQ   Sequence   446 AA;

  Query Match            96.8%;  Score 2447.5;  DB 20;  Length 446;
  Best Local Similarity  97.1%;  Pred. No. 2.4e-177;
  Matches  442;  Conservative    1;  Mismatches    3;  Indels    9;  Gaps    1;

Qy      1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db      1 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60

Qy     61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120

Qy    121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQAAIEAFVC 180

Qy    181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240

Qy    241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300

Qy    301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVI 360

Qy    361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420
          |||||||||||||||||||||||||||||||||||||||||||          ||||||||
Db    361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNH---------GFGNCVEL 411

Qy    421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
          |||||||||:|||||||||||||||||||||||||
Db    412 QASAAFNWNNQRCKTRNRYICQFAQEHISRWGPGS 446
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